

SEQUENCE LISTING

<110> OHYAMA, KANJI

<120> MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE
GENES AND USE OF THE SAME

<130> 47236-0009-00-US

<140> 10/584,082

<141> 2006-06-22

<150> PCT/JP04/19196

<151> 2004-12-22

<150> JP 2003-425673

<151> 2003-12-22

<160> 46

<170> PatentIn Ver. 3.3

<210> 1

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<213> Marchantia polymorpha

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<222> (253)..(1698)

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<212> PRT

<213> *Marchantia polymorpha*

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His	Asn	Gly	Met	Asp	Val	Tyr	Asn	Asp	Pro	Arg	Asp	Phe	Val	Thr	Ala	385	390	395
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Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Ser	420	425	430
Leu	Pro	Arg	His	Asn	Leu	Ala	Lys	Val	Ala	Pro	His	Val	Lys	Ala	Leu	435	440	445
Cys	Ala	Lys	His	Gly	Leu	His	Tyr	Glu	Glu	Leu	Ser	Leu	Gly	Thr	Gly	450	455	460

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<213> Marchantia polymorpha

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 Tyr Leu Thr Gln Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln
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 Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile
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 Lys Ser Lys Lys Ala Glu
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Ile	Lys	Asn	Asn	Ser	Pro	Tyr	Pro	Gln	Phe	Leu	Ile	Gln	Ile	Leu	Phe
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Tyr	Tyr	Met	Ile	Ser	Leu	Leu	Ala	Leu	Phe	Gly	Asn	Phe	Tyr	Val	His
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Asn His Gly Ser Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly	
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His Val Ala Gly His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro	
240 245 250	
gac att cgt gtg aag gat cct gat tta cga cgg gtt act tct caa caa	1178
Asp Ile Arg Val Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln	
255 260 265	
ccc cga aga tgg ttt cac gag tat cag cat atc tac tta gga gta ctc	1226
Pro Arg Arg Trp Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu	
270 275 280	
tat ggc gtt ctt gcc tta aaa agt gtg ttg att gat gat ttc agc gcc	1274
Tyr Gly Val Leu Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala	
285 290 295 300	
ttc ttc agt ggt gct atc ggc cca gta aag ata gct caa atg aca cca	1322
Phe Phe Ser Gly Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro	
305 310 315	
ctc gag atg ggc gtc ttc tgg gga ggg aag gtt gtg tac gca ctg tac	1370
Leu Glu Met Gly Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr	
320 325 330	

atg ttt ttg ctc cct atg atg tat ggt caa tac aac att ctt act ttc	1418
Met Phe Leu Leu Pro Met Met Tyr Gly Gln Tyr Asn Ile Leu Thr Phe	
335 340 345	
att ggt ctc tac att ctc tca cag tta gtt gca ggg tgg act ctt gcc	1466
Ile Gly Leu Tyr Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala	
350 355 360	
ctc ttc ttt caa gta gca cac gtt gtc gac gat gca gta ttt ccc gtt	1514
Leu Phe Phe Gln Val Ala His Val Val Asp Ala Val Phe Pro Val	
365 370 375 380	
gcg gaa aca gat ggt gga aaa gca aag att cct tct ggt tgg gca gaa	1562
Ala Glu Thr Asp Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu	
385 390 395	
atg cag gtc aga acc act acc aat ttc agc tca cga tca atg ttc tgg	1610
Met Gln Val Arg Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp	
400 405 410	
aca cat att agt ggc ggt ctg aac cat cag atc gag cac cat ctt ttc	1658
Thr His Ile Ser Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe	
415 420 425	
ccg ggt gtc tgt cat gtt cac tac cca agc ata cag cca atc gtg aag	1706
Pro Gly Val Cys His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys	
430 435 440	
gct acc tgt gac gag ttc aac gtg cct tat act tcc tac ccc act ttc	1754
Ala Thr Cys Asp Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe	
445 450 455 460	
tgg gcg gcc ctt agg gca cat ttt caa cat ctg aaa aac gtc gga cta	1802
Trp Ala Ala Leu Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu	
465 470 475	
caa gat gga cta cga ctg gat ggc tga actgtgacag catgctttgg	1849
Gln Asp Gly Leu Arg Leu Asp Gly	
480	
gcctgcactt tcagatttcg gatcgaaggt gcgggcatg gaaataatca gataagagtt	1909
gtaagtaacg ttcaggagga gagcagaacg gattgatgag tgtccatttg tgaggcttcc	1969
acctttcagg aacagaagtt gattcgaatg cgaaacctcc aatgagcatt tcacagccgt	2029
cttctccttg gccatcatgt gttcctccta gggagcttcg gtttttggaa gttagtcagc	2089
ttacttttoga agatcgttca acgctcaagg ctagattttg tcgacactat ttagttaggt	2149
ccgatagata ggtgataaga ttccggtgcc ctacacatg tttcatcagt tgcgatgtaa	2209
ttccagtaat ccacgtatgt ggctccagtg tctgctgaaa tcagcacagg cagctatatc	2269
atgctccttg atctctaaaa aaaaaaaaaa aaaaaaaaaa	2307

<211> 484

<212> PRT

<213> *Marchantia polymorpha*

<400> 6

Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly Pro Glu Val Phe
1 5 10 15

Arg Leu Pro Asp Asp Ala Ile Pro Ala Gln Asp Arg Arg Ser Thr Gln
20 25 30

Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn Thr Pro Asn Asp
35 40 45

Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp Val
50 55 60

Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys Ala Gly Gln Asp
65 70 75 80

Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys Leu
85 90 95

Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser Ala Gly Asp Glu
100 105 110

Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu Glu His Glu Val
115 120 125

Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr Phe Arg Lys Gln
130 135 140

Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val Lys Ser Ala Val
145 150 155 160

Ile Ile Gly Thr Leu Leu Leu Cys Tyr Tyr Phe Gly Phe Phe Trp Ser
165 170 175

Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile Met Gly Phe Cys
180 185 190

Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly Asn His Gly Ser
195 200 205

Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly Ala Thr Leu Asp
210 215 220

Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Ala Gly
225 230 235 240

His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro Asp Ile Arg Val
245 250 255

Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln Pro Arg Arg Trp
260 265 270

Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu Tyr Gly Val Leu
275 280 285

Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala Phe Phe Ser Gly
 290 295 300
 Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro Leu Glu Met Gly
 305 310 315 320
 Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr Met Phe Leu Leu
 325 330 335
 Pro Met Met Tyr Gly Gln Tyr Asn Ile Leu Thr Phe Ile Gly Leu Tyr
 340 345 350
 Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala Leu Phe Phe Gln
 355 360 365
 Val Ala His Val Val Asp Asp Ala Val Phe Pro Val Ala Glu Thr Asp
 370 375 380
 Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu Met Gln Val Arg
 385 390 395 400
 Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp Thr His Ile Ser
 405 410 415
 Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro Gly Val Cys
 420 425 430
 His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys Ala Thr Cys Asp
 435 440 445
 Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe Trp Ala Ala Leu
 450 455 460
 Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu Gln Asp Gly Leu
 465 470 475 480
 Arg Leu Asp Gly

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> modified_base

<222> (12)

<223> a, c, g, t, unknown or other

<400> 7

tggtggaarg anaarcayaa

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (4)
 <223> inosine

<220>
 <221> modified_base
 <222> (7)
 <223> inosine

<220>
 <221> modified_base
 <222> (10)
 <223> inosine

<220>
 <221> modified_base
 <222> (13)
 <223> inosine

<400> 8
 rtttnarnccn ccngtraacc a

21

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 9
 aagttgcctt cgatgtttct gg

22

<210> 10
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 10
 gctcgctgg agcaaggaaa tc

22

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (3)
 <223> inosine

<220>
 <221> modified_base
 <222> (18)
 <223> inosine

<400> 11
 gtngarttya tggayacngt

20

<210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (3)
 <223> inosine

<220>
 <221> modified_base
 <222> (12)
 <223> inosine

<400> 12
 ckncccccara anarrtaytt

20

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 13
gcgagctttc tcgttctttc cc 22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 14
tatgattttg aagcgcaaca cg 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (6)
<223> inosine

<220>
<221> modified_base
<222> (9)
<223> inosine

<220>
<221> modified_base
<222> (14)
<223> inosine

<400> 15
athrangrna artntaygay gt 22

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
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<222> (3)
<223> inosine

<220>
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 <222> (6)
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<220>
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 <222> (9)
 <223> inosine

<220>
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 <222> (18)
 <223> inosine

<400> 16
 ggnaynkwnt sdatrtcngg rtc

23

<210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 17
 gtgtgtacga tccgtgggta cc

22

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 18
 aaggcgggac aggattcaac ac

22

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 19
 ggaattcgcg atggcctcgt ccaccaccac

30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 20
ggaattctac ttctgcagcg tatgctacc 29

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 21
ggaattcgcg atggagggcg acgagatgg 29

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 22
ggaattcttc tgcctttttg ctcttgatc 29

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 23
gttgaattcg acagttatgc cgccacacgc 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 24
 gttgaattca ggcccaaagc atgctgtcac 30

 <210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 25
 cgggatcctc tcctggcgca ccatcgtc 28

 <210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 26
 ggggtaccaa cgcgctttcc caccaacg 28

 <210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
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 primer

 <400> 27
 gctctagagc gatggcctcg tccaccacc 29

 <210> 28
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
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 primer

 <400> 28
 gctctagact atactttcgc agcgtatgc 29

<210> 29
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 29
 gctctagagc gatggaggcg tacgagatgg

30

<210> 30
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 30
 gctctagatt attctgcctt ttgctc

27

<210> 31
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 31
 gctctagaga cagttatgcc gccacacgc

29

<210> 32
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 32
 gctctagaag gcccaaagca tgctgtcac

29

<210> 33
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 33
caggaaacag ctatgacc 18

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 34
aaactgcaga ttcccgatct agtaacatag 30

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 35
ccggaattcg catgcctgca ggtccccaga 30

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 36
tgtaaaacga cggccagt 18

<210> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (4)
<223> Glu or Asp

<400> 37
Trp Trp Lys Xaa Lys His Asn
1 5

<210> 38
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 38
Trp Phe Thr Gly Gly Leu Asn
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Val Glu Phe Met Asp Thr Val
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 40
Lys Tyr Leu Phe Trp Gly Arg
1 5

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (2)
 <223> Glu or Asn

<220>
 <221> MOD_RES
 <222> (3)
 <223> Gly or Asp

<400> 41
 Ile Xaa Xaa Lys Val Tyr Asp Val
 1 5

<210> 42
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <221> MOD_RES
 <222> (5)
 <223> Gln or Asp

<220>
 <221> MOD_RES
 <222> (6)
 <223> Tyr or Thr

<220>
 <221> MOD_RES
 <222> (7)
 <223> Met or Val

<400> 42
 Asp Pro Asp Ile Xaa Xaa Xaa Pro
 1 5

<210> 43
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 43
agtctctaga gcgatggagg cgtacg 26

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 44
cagtgaagctc ggtgtcttat tctgcc 26

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 45
agcttctaga gccatgccgc cacacgccc 29

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 46
cagtgaagctc tcagccatcc agtcgt 26